

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/59/490
Source: IFWP
Date Processed by STIC: 9/18/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 09/18/2006

PATENT APPLICATION: US/10/591,490

TIME: 15:26:44

Input Set : A:\SHIMIZU-13116_sq.txt

Output Set: N:\CRF4\09182006\J591490.raw

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3 <110> APPLICANT: KADOWAKI, Takashi
4     YAMAUCHI, Toshimasa
6 <120> TITLE OF INVENTION: REGULATOR FOR ADIPONECTIN RECEPTOR EXPRESSION
8 <130> FILE REFERENCE: SHIMIZU-13116
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/591,490
C--> 10 <141> CURRENT FILING DATE: 2006-09-01
10 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/003744
11 <151> PRIOR FILING DATE: 2005-03-04
13 <150> PRIOR APPLICATION NUMBER: US 60/549,561
14 <151> PRIOR FILING DATE: 2004-03-04
16 <160> NUMBER OF SEQ ID NOS: 15
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 652
22 <212> TYPE: PRT
23 <213> ORGANISM: Mus musculus
25 <400> SEQUENCE: 1
27 Met Ala Glu Ala Pro Gln Val Val Glu Thr Asp Pro Asp Phe Glu Pro
28 1          5          10          15
31 Leu Pro Arg Gln Arg Ser Cys Thr Trp Pro Leu Pro Arg Pro Glu Phe
32          20          25          30
35 Asn Gln Ser Asn Ser Thr Thr Ser Ser Pro Ala Pro Ser Gly Gly Ala
36          35          40          45
39 Ala Ala Asn Pro Asp Ala Ala Ala Ser Leu Ala Ser Ala Ser Ala Val
40          50          55          60
43 Ser Thr Asp Phe Met Ser Asn Leu Ser Leu Leu Glu Glu Ser Glu Asp
44 65          70          75          80
47 Phe Ala Arg Ala Pro Gly Cys Val Ala Val Ala Ala Ala Ala Ala
48          85          90          95
51 Ser Arg Gly Leu Cys Gly Asp Phe Gln Gly Pro Glu Ala Gly Cys Val
52          100         105         110
55 His Pro Ala Pro Pro Gln Pro Pro Pro Thr Gly Pro Leu Ser Gln Pro
56          115         120         125
59 Pro Pro Val Pro Pro Ser Ala Ala Ala Ala Ala Gly Pro Leu Ala Gly
60          130         135         140
63 Gln Pro Arg Lys Thr Ser Ser Ser Arg Arg Asn Ala Trp Gly Asn Leu
64 145         150         155         160
67 Ser Tyr Ala Asp Leu Ile Thr Lys Ala Ile Glu Ser Ser Ala Glu Lys
68          165         170         175
71 Arg Leu Thr Leu Ser Gln Ile Tyr Glu Trp Met Val Lys Ser Val Pro
72          180         185         190
75 Tyr Phe Lys Asp Lys Gly Asp Ser Asn Ser Ser Ala Gly Trp Lys Asn
76          195         200         205

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79 Ser Ile Arg His Asn Leu Ser Leu His Ser Lys Phe Ile Arg Val Gln
80      210                      215                      220
83 Asn Glu Gly Thr Gly Lys Ser Ser Trp Trp Met Leu Asn Pro Glu Gly
84 225                      230                      235                      240
87 Gly Lys Ser Gly Lys Ser Pro Arg Arg Arg Ala Ala Ser Met Asp Asn
88                      245                      250                      255
91 Asn Ser Lys Phe Ala Lys Ser Arg Gly Arg Ala Ala Lys Lys Lys Ala
92      260                      265                      270
95 Ser Leu Gln Ser Gly Gln Glu Gly Pro Gly Asp Ser Pro Gly Ser Gln
96      275                      280                      285
99 Phe Ser Lys Trp Pro Ala Ser Pro Gly Ser His Ser Asn Asp Asp Phe
100     290                      295                      300
103 Asp Asn Trp Ser Thr Phe Arg Pro Arg Thr Ser Ser Asn Ala Ser Thr
104 305                      310                      315                      320
107 Ile Ser Gly Arg Leu Ser Pro Ile Met Thr Glu Gln Asp Asp Leu Gly
108                      325                      330                      335
111 Asp Gly Asp Val His Ser Leu Val Tyr Pro Pro Ser Ala Ala Lys Met
112     340                      345                      350
115 Ala Ser Thr Leu Pro Ser Leu Ser Glu Ile Ser Asn Pro Glu Asn Met
116     355                      360                      365
119 Glu Asn Leu Leu Asp Asn Leu Asn Leu Leu Ser Ser Pro Thr Ser Leu
120     370                      375                      380
123 Thr Val Ser Thr Gln Ser Ser Pro Gly Ser Met Met Gln Gln Thr Pro
124 385                      390                      395                      400
127 Cys Tyr Ser Phe Ala Pro Pro Asn Thr Ser Leu Asn Ser Pro Ser Pro
128     405                      410                      415
131 Asn Tyr Ser Lys Tyr Thr Tyr Gly Gln Ser Ser Met Ser Pro Leu Pro
132     420                      425                      430
135 Gln Met Pro Met Gln Thr Leu Gln Asp Ser Lys Ser Ser Tyr Gly Gly
136     435                      440                      445
139 Leu Asn Gln Tyr Asn Cys Ala Pro Gly Leu Leu Lys Glu Leu Leu Thr
140     450                      455                      460
143 Ser Asp Ser Pro Pro His Asn Asp Ile Met Ser Pro Val Asp Pro Gly
144 465                      470                      475                      480
147 Val Ala Gln Pro Asn Ser Arg Val Leu Gly Gln Asn Val Met Met Gly
148     485                      490                      495
151 Pro Asn Ser Val Met Pro Ala Tyr Gly Ser Gln Ala Ser His Asn Lys
152     500                      505                      510
155 Met Met Asn Pro Ser Ser His Thr His Pro Gly His Ala Gln Gln Thr
156     515                      520                      525
159 Ala Ser Val Asn Gly Arg Thr Leu Pro His Val Val Asn Thr Met Pro
160     530                      535                      540
163 His Thr Ser Ala Met Asn Arg Leu Thr Pro Val Lys Thr Pro Leu Gln
164 545                      550                      555                      560
167 Val Pro Leu Ser His Pro Met Gln Met Ser Ala Leu Gly Ser Tyr Ser
168     565                      570                      575
171 Ser Val Ser Ser Cys Asn Gly Tyr Gly Arg Met Gly Val Leu His Gln
172     580                      585                      590
175 Glu Lys Leu Pro Ser Asp Leu Asp Gly Met Phe Ile Glu Arg Leu Asp

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176          595          600          605
179 Cys Asp Met Glu Ser Ile Ile Arg Asn Asp Pro Met Asp Gly Asp Thr
180          610          615          620
183 Leu Asp Phe Asn Phe Asp Asn Val Leu Pro Asn Gln Ser Phe Pro His
184 625          630          635          640
187 Ser Val Lys Thr Thr Thr His Ser Trp Val Ser Gly
188          645          650
191 <210> SEQ ID NO: 2
192 <211> LENGTH: 2103
193 <212> TYPE: DNA
194 <213> ORGANISM: Mus musculus
197 <220> FEATURE:
198 <221> NAME/KEY: CDS
199 <222> LOCATION: (7)..(1965)
201 <400> SEQUENCE: 2
202 gtcacc atg gcc gag gcg ccc cag gtg gtg gag acc gac ccg gac ttc      48
203      Met Ala Glu Ala Pro Gln Val Val Glu Thr Asp Pro Asp Phe
204      1          5          10
206 gag ccg atg gcc cgg cag cgc tcc tgt acc tgg ccg ctg ccc agg ccg      96
207 Glu Pro Leu Pro Arg Gln Arg Ser Cys Thr Trp Pro Leu Pro Arg Pro
208 15          20          25          30
210 gag ttt aac cag tcc aac tcg acc acc tcc agt ccg gcg ccg tcg ggc      144
211 Glu Phe Asn Gln Ser Asn Ser Thr Thr Ser Ser Pro Ala Pro Ser Gly
212          35          40          45
214 ggc gcg gcc gcc aac ccc gac gcc gcg gcg agc ctg gcc tcg gcg tcc      192
215 Gly Ala Ala Ala Asn Pro Asp Ala Ala Ala Ser Leu Ala Ser Ala Ser
216          50          55          60
218 gct gtc agc acc gac ttt atg agc aac ctg agc ctg ctg gag gag agt      240
219 Ala Val Ser Thr Asp Phe Met Ser Asn Leu Ser Leu Leu Glu Glu Ser
220          65          70          75
222 gag gac ttc gcg cgg gcg cca ggc tgc gtg gcc gtg gcg gcg gcg gct      288
223 Glu Asp Phe Ala Arg Ala Pro Gly Cys Val Ala Val Ala Ala Ala Ala
224          80          85          90
226 gcg gcc agc agg ggc ctg tgc ggg gac ttc cag ggc ccc gag gcg ggc      336
227 Ala Ala Ser Arg Gly Leu Cys Gly Asp Phe Gln Gly Pro Glu Ala Gly
228 95          100          105          110
230 tgc gtg cac cca gcg ccg cca cag ccc cca ccg acc ggg ccg ctg tcg      384
231 Cys Val His Pro Ala Pro Pro Gln Pro Pro Pro Thr Gly Pro Leu Ser
232          115          120          125
234 cag ccc cca ccc gtg cct ccc tcc gct gcc gcc gcc gcg ggg cca ctc      432
235 Gln Pro Pro Pro Val Pro Pro Ser Ala Ala Ala Ala Ala Gly Pro Leu
236          130          135          140
238 gcg gga cag ccg cgc aag acc agc tcg tcg cgc cgc aac gcg tgg ggc      480
239 Ala Gly Gln Pro Arg Lys Thr Ser Ser Ser Arg Arg Asn Ala Trp Gly
240          145          150          155
242 aac ctg tcg tac gcc gac ctc atc acc aag gcc atc gag agc tca gcc      528
243 Asn Leu Ser Tyr Ala Asp Leu Ile Thr Lys Ala Ile Glu Ser Ser Ala
244          160          165          170
246 gag aag agg ctc acc ctg tcg cag atc tac gag tgg atg gtg aag agc      576

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247	Glu	Lys	Arg	Leu	Thr	Leu	Ser	Gln	Ile	Tyr	Glu	Trp	Met	Val	Lys	Ser	
248	175					180					185					190	
250	gtg	ccc	tac	ttc	aag	gat	aag	ggc	gac	agc	aac	agc	tcg	gcg	ggc	tgg	624
251	Val	Pro	Tyr	Phe	Lys	Asp	Lys	Gly	Asp	Ser	Asn	Ser	Ser	Ala	Gly	Trp	
252				195					200						205		
254	aag	aat	tca	att	cgc	cac	aat	ctg	tcc	ctt	cac	agc	aag	ttt	att	cga	672
255	Lys	Asn	Ser	Ile	Arg	His	Asn	Leu	Ser	Leu	His	Ser	Lys	Phe	Ile	Arg	
256				210					215					220			
258	gtg	cag	aat	gaa	gga	act	gga	aag	agt	tct	tgg	tgg	atg	ctc	aat	cca	720
259	Val	Gln	Asn	Glu	Gly	Thr	Gly	Lys	Ser	Ser	Trp	Trp	Met	Leu	Asn	Pro	
260			225						230					235			
262	gag	gga	ggc	aag	agc	gga	aaa	tca	ccc	cgg	aga	aga	gct	gcg	tcc	atg	768
263	Glu	Gly	Gly	Lys	Ser	Gly	Lys	Ser	Pro	Arg	Arg	Arg	Ala	Ala	Ser	Met	
264		240					245						250				
266	gac	aac	aac	agt	aaa	ttt	gct	aag	agc	cga	ggg	cgg	gct	gct	aag	aaa	816
267	Asp	Asn	Asn	Ser	Lys	Phe	Ala	Lys	Ser	Arg	Gly	Arg	Ala	Ala	Lys	Lys	
268	255				260					265						270	
270	aaa	gca	tct	ctc	cag	tct	ggg	caa	gag	ggt	cct	gga	gac	agc	cct	ggg	864
271	Lys	Ala	Ser	Leu	Gln	Ser	Gly	Gln	Glu	Gly	Pro	Gly	Asp	Ser	Pro	Gly	
272				275						280					285		
274	tct	cag	ttt	tct	aag	tgg	cct	gcg	agt	cct	ggg	tcc	cac	agc	aac	gat	912
275	Ser	Gln	Phe	Ser	Lys	Trp	Pro	Ala	Ser	Pro	Gly	Ser	His	Ser	Asn	Asp	
276			290						295					300			
278	gac	ttt	gat	aac	tgg	agt	aca	ttt	cgt	cct	cga	acc	agc	tca	aat	gct	960
279	Asp	Phe	Asp	Asn	Trp	Ser	Thr	Phe	Arg	Pro	Arg	Thr	Ser	Ser	Asn	Ala	
280			305						310					315			
282	agt	acc	atc	agt	ggg	aga	ctt	tct	ccc	atc	atg	aca	gag	cag	gat	gac	1008
283	Ser	Thr	Ile	Ser	Gly	Arg	Leu	Ser	Pro	Ile	Met	Thr	Glu	Gln	Asp	Asp	
284		320					325					330					
286	ctg	gga	gat	ggg	gac	gtg	cat	tcc	ctg	gtg	tat	cca	ccc	tct	gct	gcc	1056
287	Leu	Gly	Asp	Gly	Asp	Val	His	Ser	Leu	Val	Tyr	Pro	Pro	Ser	Ala	Ala	
288	335					340					345					350	
290	aag	atg	gcg	tct	acg	ctg	ccc	agt	ctg	tct	gaa	atc	agc	aat	cca	gaa	1104
291	Lys	Met	Ala	Ser	Thr	Leu	Pro	Ser	Leu	Ser	Glu	Ile	Ser	Asn	Pro	Glu	
292				355						360					365		
294	aac	atg	gag	aac	ctt	ctg	gat	aat	ctc	aac	ctt	ctc	tcg	tcc	cca	aca	1152
295	Asn	Met	Glu	Asn	Leu	Leu	Asp	Asn	Leu	Asn	Leu	Leu	Ser	Ser	Pro	Thr	
296			370						375					380			
298	tct	tta	act	gtg	tcc	acc	cag	tcc	tcg	cct	ggc	agc	atg	atg	cag	cag	1200
299	Ser	Leu	Thr	Val	Ser	Thr	Gln	Ser	Ser	Pro	Gly	Ser	Met	Met	Gln	Gln	
300			385						390					395			
302	aca	cca	tgc	tat	tcg	ttt	gca	ccg	cca	aac	acc	agt	cta	aat	tca	ccc	1248
303	Thr	Pro	Cys	Tyr	Ser	Phe	Ala	Pro	Pro	Asn	Thr	Ser	Leu	Asn	Ser	Pro	
304		400					405						410				
306	agt	cca	aac	tac	tca	aag	tac	aca	tac	ggc	caa	tcc	agc	atg	agc	cct	1296
307	Ser	Pro	Asn	Tyr	Ser	Lys	Tyr	Thr	Tyr	Gly	Gln	Ser	Ser	Met	Ser	Pro	
308	415					420					425					430	
310	ttg	ccc	cag	atg	cct	atg	cag	aca	ctt	cag	gac	agc	aaa	tca	agt	tac	1344
311	Leu	Pro	Gln	Met	Pro	Met	Gln	Thr	Leu	Gln	Asp	Ser	Lys	Ser	Ser	Tyr	

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312          435          440          445
314 gga gga ttg aac cag tat aac tgt gcc cca gga ctc ttg aaa gag ttg      1392
315 Gly Gly Leu Asn Gln Tyr Asn Cys Ala Pro Gly Leu Leu Lys Glu Leu
316          450          455          460
318 ttg act tct gac tct cct ccc cac aat gac att atg tca ccg gtt gat      1440
319 Leu Thr Ser Asp Ser Pro Pro His Asn Asp Ile Met Ser Pro Val Asp
320          465          470          475
322 ccc gga gtg gcc caa ccc aac agt cgg gtc ctg ggc caa aat gta atg      1488
323 Pro Gly Val Ala Gln Pro Asn Ser Arg Val Leu Gly Gln Asn Val Met
324          480          485          490
326 atg ggc cct aat tcg gtc atg cca gcg tat ggc agc cag gca tct cat      1536
327 Met Gly Pro Asn Ser Val Met Pro Ala Tyr Gly Ser Gln Ala Ser His
328 495          500          505          510
330 aac aaa atg atg aac ccc agc tcc cac acc cac cct gga cat gca cag      1584
331 Asn Lys Met Met Asn Pro Ser Ser His Thr His Pro Gly His Ala Gln
332          515          520          525
334 caa acg gct tcg gtc aac ggc cgt acc ctg ccc cat gtg gtg aac acc      1632
335 Gln Thr Ala Ser Val Asn Gly Arg Thr Leu Pro His Val Val Asn Thr
336          530          535          540
338 atg cct cac aca tct gcc atg aac cgc ttg acc ccc gtg aag aca cct      1680
339 Met Pro His Thr Ser Ala Met Asn Arg Leu Thr Pro Val Lys Thr Pro
340          545          550          555
342 tta caa gtg cct ctg tcc cac ccc atg cag atg agt gcc ctg ggc agc      1728
343 Leu Gln Val Pro Leu Ser His Pro Met Gln Met Ser Ala Leu Gly Ser
344          560          565          570
346 tac tcc tcg gtg agc agc tgc aat ggc tat ggt agg atg ggt gtc ctc      1776
347 Tyr Ser Ser Val Ser Ser Cys Asn Gly Tyr Gly Arg Met Gly Val Leu
348 575          580          585          590
350 cac cag gag aag ctc cca agt gac ttg gat ggc atg ttt att gag cgc      1824
351 His Gln Glu Lys Leu Pro Ser Asp Leu Asp Gly Met Phe Ile Glu Arg
352          595          600          605
354 ttg gac tgt gac atg gag tcc atc att cgg aat gac ccc atg gat gga      1872
355 Leu Asp Cys Asp Met Glu Ser Ile Ile Arg Asn Asp Pro Met Asp Gly
356          610          615          620
358 gat acc ttg gat ttt aac ttt gat aat gtg ttg ccc aac caa agc ttc      1920
359 Asp Thr Leu Asp Phe Asn Phe Asp Asn Val Leu Pro Asn Gln Ser Phe
360          625          630          635
362 cca cac agt gtc aag act aca aca cac agc tgg gtg tca ggc taa      1965
363 Pro His Ser Val Lys Thr Thr Thr His Ser Trp Val Ser Gly
364          640          645          650
366 gagtttagtg agcaggctac atttaaaagt ccttcagatt gtctgacagc aggaactgag      2025
368 gagcagtcca aagatgccct tcacccctcc ttatagtttt caagattaaa aaaaaaaaaa      2085
370 aaaaaaaaaa aaaaaaaaaa      2103
374 <210> SEQ ID NO: 3
375 <211> LENGTH: 652
376 <212> TYPE: PRT
377 <213> ORGANISM: Mus musculus
379 <400> SEQUENCE: 3
381 Met Ala Glu Ala Pro Gln Val Val Glu Thr Asp Pro Asp Phe Glu Pro

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\SHIMIZU-13116_sq.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:10,11,12,13,14,15

VERIFICATION SUMMARY

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Input Set : A:\SHIMIZU-13116_sq.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date